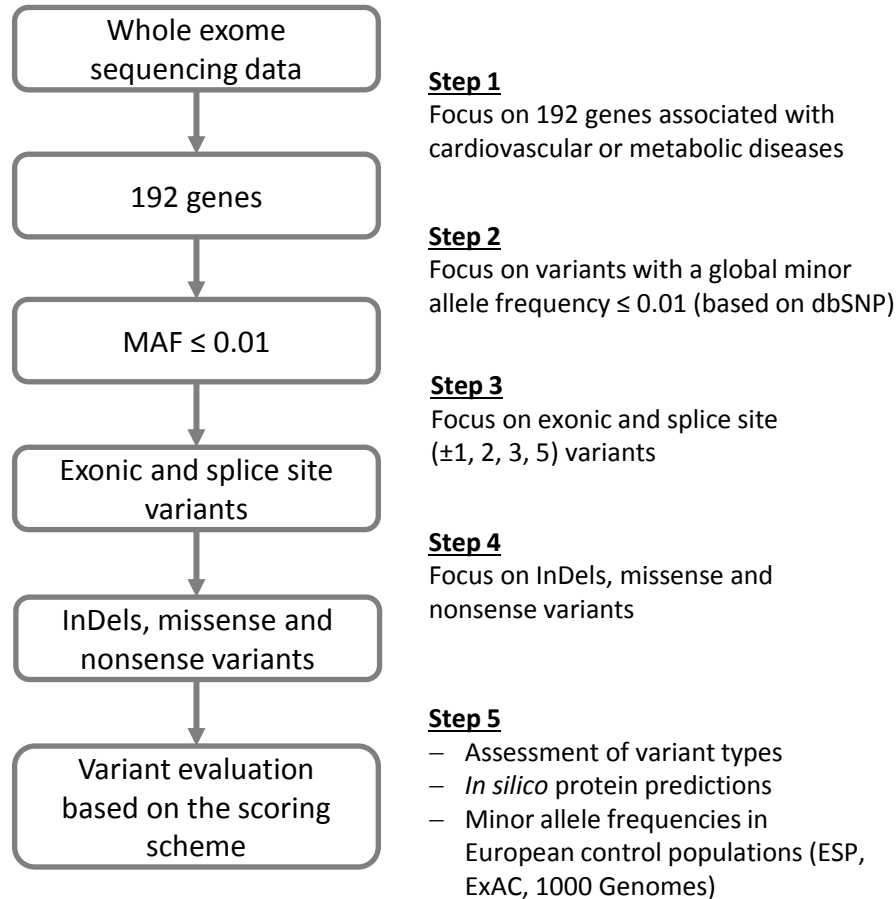


Neubauer, *et al.* Post-mortem whole exome analysis in a large sudden infant death syndrome cohort with a focus on cardiovascular and metabolic genetic diseases



Supp. Data Figure S1 Filtering flow chart (adapted from Neubauer, *et al.*²⁸)

Whole exome sequencing data were filtered for 192 genes associated with cardiovascular and metabolic diseases. The filtering steps focused on a global MAF less than 0.01 (step 2), exonic and splice site variants (step 3), InDels, missense and nonsense variants (step 4), and variant evaluation based on the scoring scheme (step 5).

InDels: insertions and deletions, MAF: minor allele frequency